FIG. 1

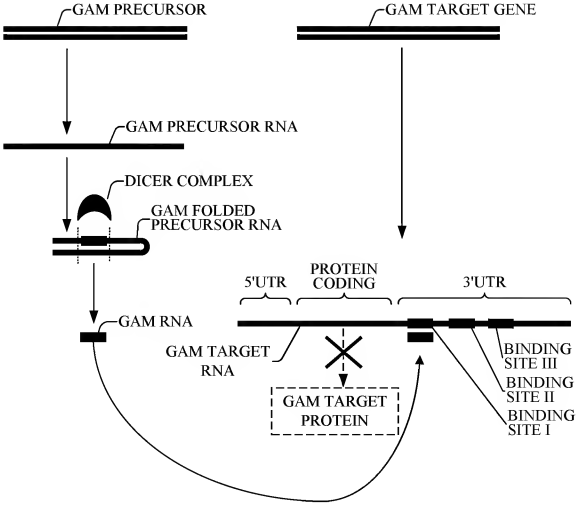

GAM PRECURSOR
GAM TARGET GENE
GAM PRECURSOR RNA
DICER COMPLEX
GAM FOLDED
PRECURSOR RNA
5'UTR
PROTEIN
CODING
3'UTR
GAM RNA
GAM TARGET
RNA
BINDING
SITE III
BINDING
SITE II
BINDING
SITE I
GAM TARGET
PROTEIN

FIG. 2

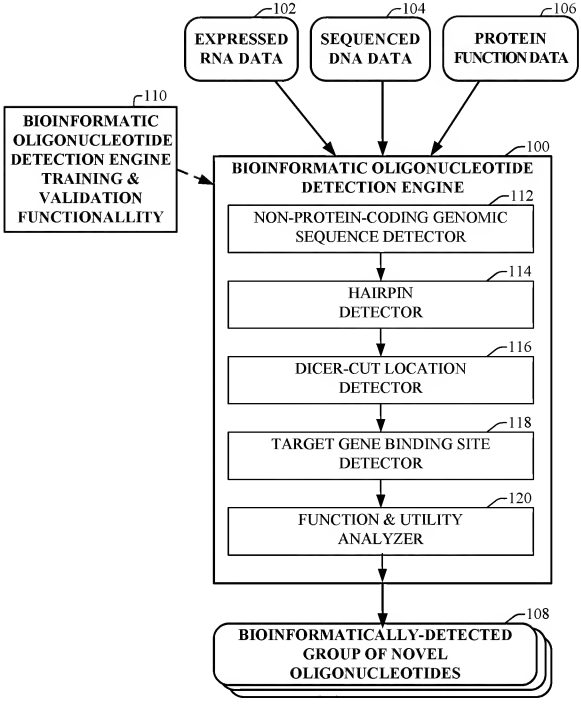

102
EXPRESSED RNA DATA
104
SEQUENCED DNA DATA
106
PROTEIN FUNCTION DATA
110
BIOINFORMATIC OLIGONUCLEOTIDE DETECTION ENGINE TRAINING & VALIDATION FUNCTIONALLITY
100
BIOINFORMATIC OLIGONUCLEOTIDE DETECTION ENGINE
112
NON-PROTEIN-CODING GENOMIC SEQUENCE DETECTOR
114
HAIRPIN DETECTOR
116
DICER-CUT LOCATION DETECTOR
118
TARGET GENE BINDING SITE DETECTOR
120
FUNCTION & UTILITY ANALYZER
108
BIOINFORMATICALLY-DETECTED GROUP OF NOVEL OLIGONUCLEOTIDES

FIG. 3

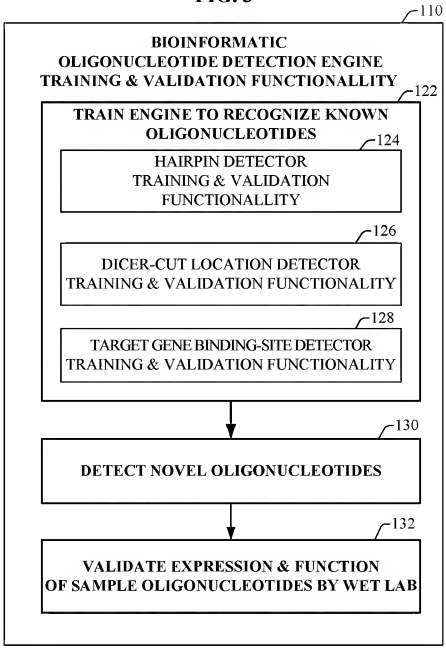

110
BIOINFORMATIC
OLIGONUCLEOTIDE DETECTION ENGINE
TRAINING & VALIDATION FUNCTIONALLITY
122
TRAIN ENGINE TO RECOGNIZE KNOWN
OLIGONUCLEOTIDES
124
HAIRPIN DETECTOR
TRAINING & VALIDATION
FUNCTIONALLITY
126
DICER-CUT LOCATION DETECTOR
TRAINING & VALIDATION FUNCTIONALITY
128
TARGET GENE BINDING-SITE DETECTOR
TRAINING & VALIDATION FUNCTIONALITY
130
DETECT NOVEL OLIGONUCLEOTIDES
132
VALIDATE EXPRESSION & FUNCTION
OF SAMPLE OLIGONUCLEOTIDES BY WET LAB

FIG. 4A

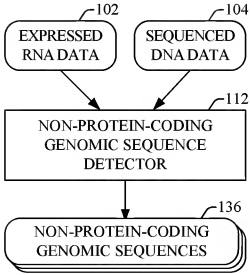

102
EXPRESSED RNA DATA
104
SEQUENCED DNA DATA
112
NON-PROTEIN-CODING GENOMIC SEQUENCE DETECTOR
136
NON-PROTEIN-CODING GENOMIC SEQUENCES

FIG. 4B

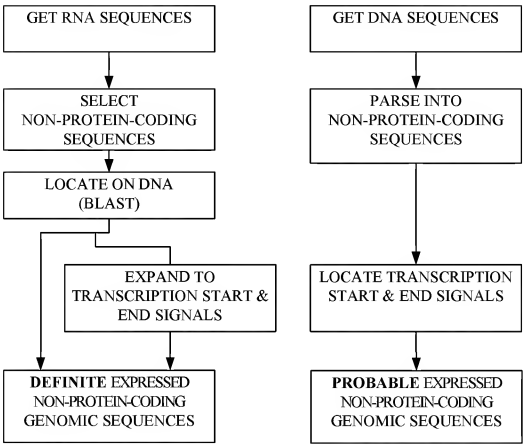

GET RNA SEQUENCES
SELECT NON-PROTEIN-CODING SEQUENCES
LOCATE ON DNA (BLAST)
EXPAND TO TRANSCRIPTION START & END SIGNALS
DEFINITE EXPRESSED NON-PROTEIN-CODING GENOMIC SEQUENCES
GET DNA SEQUENCES
PARSE INTO NON-PROTEIN-CODING SEQUENCES
LOCATE TRANSCRIPTION START & END SIGNALS
PROBABLE EXPRESSED NON-PROTEIN-CODING GENOMIC SEQUENCES

FIG. 5A

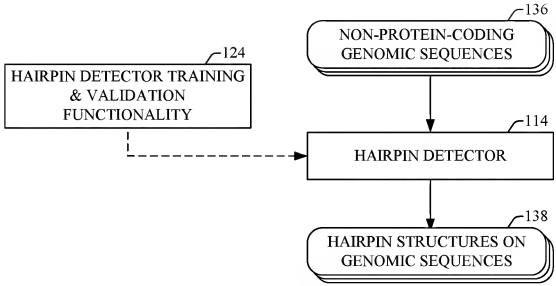

136
NON-PROTEIN-CODING GENOMIC SEQUENCES
124
HAIRPIN DETECTOR TRAINING & VALIDATION FUNCTIONALITY
114
HAIRPIN DETECTOR
138
HAIRPIN STRUCTURES ON GENOMIC SEQUENCES

FIG. 5B

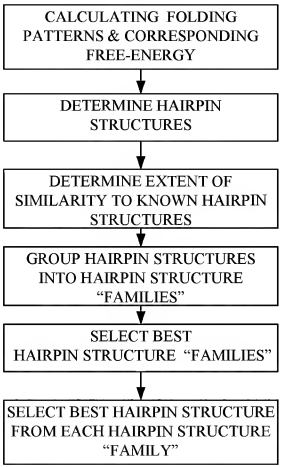

CALCULATING FOLDING PATTERNS & CORRESPONDING FREE-ENERGY
DETERMINE HAIRPIN STRUCTURES
DETERMINE EXTENT OF SIMILARITY TO KNOWN HAIRPIN STRUCTURES
GROUP HAIRPIN STRUCTURES INTO HAIRPIN STRUCTURE "FAMILIES"
SELECT BEST HAIRPIN STRUCTURE "FAMILIES"
SELECT BEST HAIRPIN STRUCTURE FROM EACH HAIRPIN STRUCTURE "FAMILY"

FIG. 6A

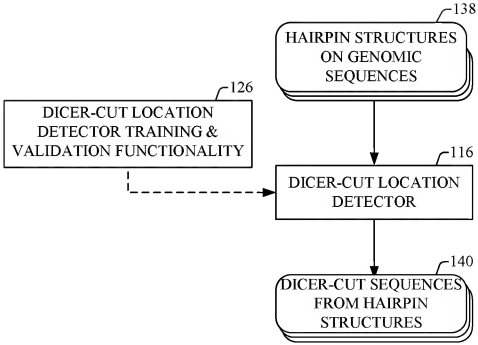

138
HAIRPIN STRUCTURES ON GENOMIC SEQUENCES
126
DICER-CUT LOCATION DETECTOR TRAINING & VALIDATION FUNCTIONALITY
116
DICER-CUT LOCATION DETECTOR
140
DICER-CUT SEQUENCES FROM HAIRPIN STRUCTURES

FIG. 6B

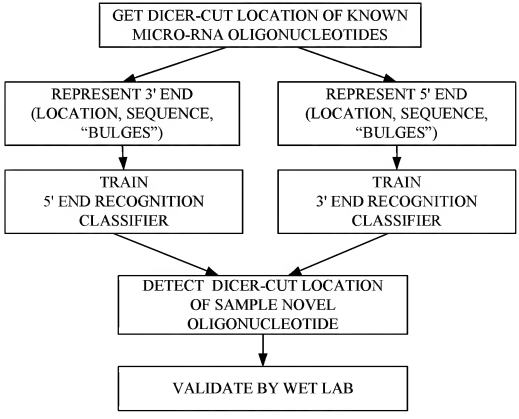

GET DICER-CUT LOCATION OF KNOWN MICRO-RNA OLIGONUCLEOTIDES
REPRESENT 3' END (LOCATION, SEQUENCE, "BULGES")
REPRESENT 5' END (LOCATION, SEQUENCE, "BULGES")
TRAIN 5' END RECOGNITION CLASSIFIER
TRAIN 3' END RECOGNITION CLASSIFIER
DETECT DICER-CUT LOCATION OF SAMPLE NOVEL OLIGONUCLEOTIDE
VALIDATE BY WET LAB

FIG. 6C

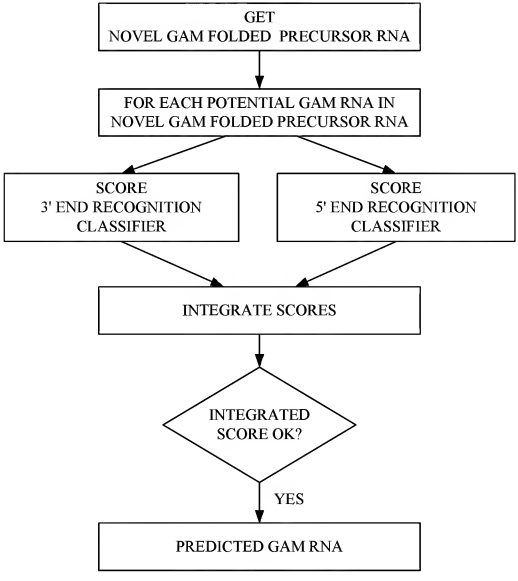

GET
NOVEL GAM FOLDED PRECURSOR RNA
FOR EACH POTENTIAL GAM RNA IN
NOVEL GAM FOLDED PRECURSOR RNA
SCORE
3' END RECOGNITION
CLASSIFIER
SCORE
5' END RECOGNITION
CLASSIFIER
INTEGRATE SCORES
INTEGRATED
SCORE OK?
YES
PREDICTED GAM RNA

FIG. 7A

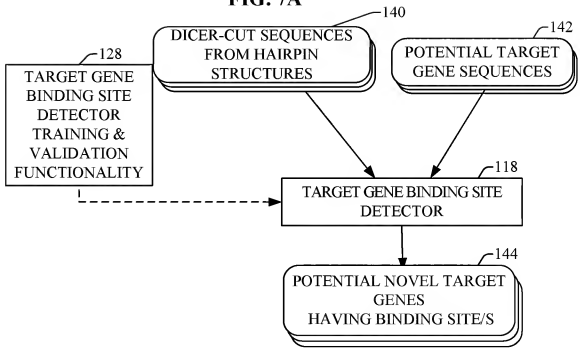

140
DICER-CUT SEQUENCES FROM HAIRPIN STRUCTURES
142
POTENTIAL TARGET GENE SEQUENCES
128
TARGET GENE BINDING SITE DETECTOR TRAINING & VALIDATION FUNCTIONALITY
118
TARGET GENE BINDING SITE DETECTOR
144
POTENTIAL NOVEL TARGET GENES HAVING BINDING SITE/S

FIG. 7B

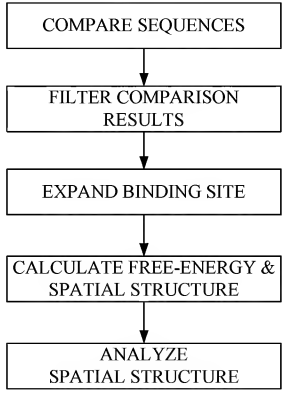

COMPARE SEQUENCES
FILTER COMPARISON RESULTS
EXPAND BINDING SITE
CALCULATE FREE-ENERGY & SPATIAL STRUCTURE
ANALYZE SPATIAL STRUCTURE

FIG. 8

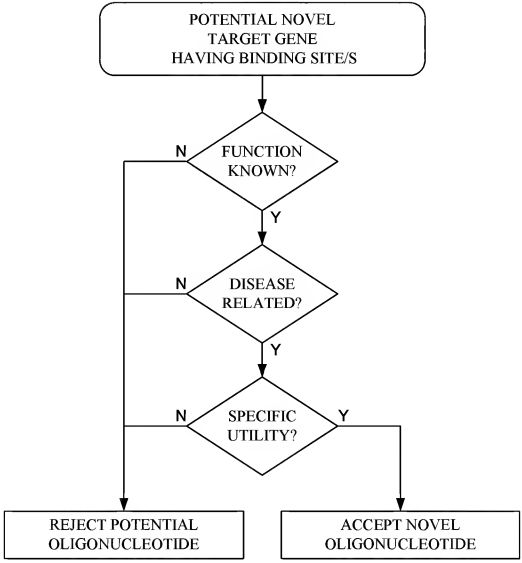

POTENTIAL NOVEL
TARGET GENE
HAVING BINDING SITE/S
FUNCTION
KNOWN?
N
Y
DISEASE
RELATED?
N
Y
SPECIFIC
UTILITY?
N
Y
REJECT POTENTIAL
OLIGONUCLEOTIDE
ACCEPT NOVEL
OLIGONUCLEOTIDE

FIG. 9

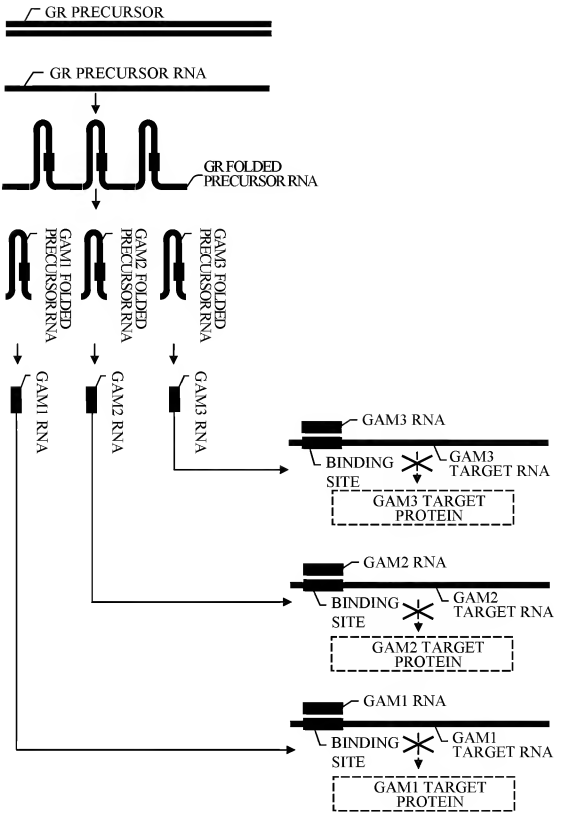

GR PRECURSOR
GR PRECURSOR RNA
GR FOLDED PRECURSOR RNA
GAM1 FOLDED PRECURSOR RNA
GAM2 FOLDED PRECURSOR RNA
GAM3 FOLDED PRECURSOR RNA
GAM1 RNA
GAM2 RNA
GAM3 RNA
GAM3 RNA
BINDING SITE
GAM3 TARGET RNA
GAM3 TARGET PROTEIN
GAM2 RNA
BINDING SITE
GAM2 TARGET RNA
GAM2 TARGET PROTEIN
GAM1 RNA
BINDING SITE
GAM1 TARGET RNA
GAM1 TARGET PROTEIN

FIG. 10

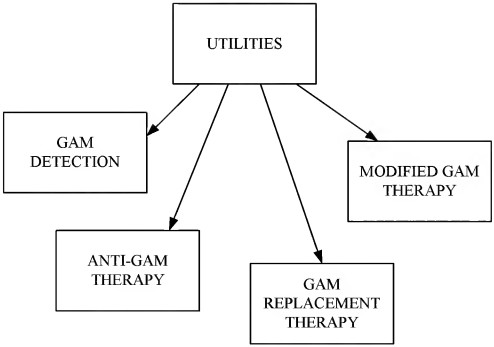

UTILITIES
GAM DETECTION
ANTI-GAM THERAPY
GAM REPLACEMENT THERAPY
MODIFIED GAM THERAPY

FIG. 11A

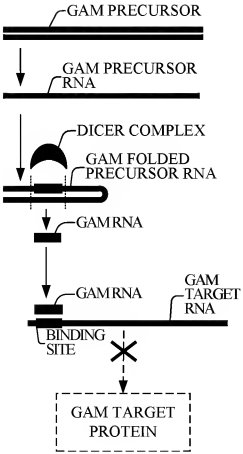


FIG. 11B

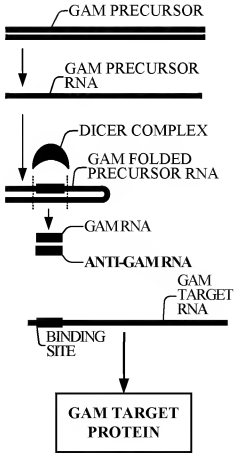


FIG. 12A

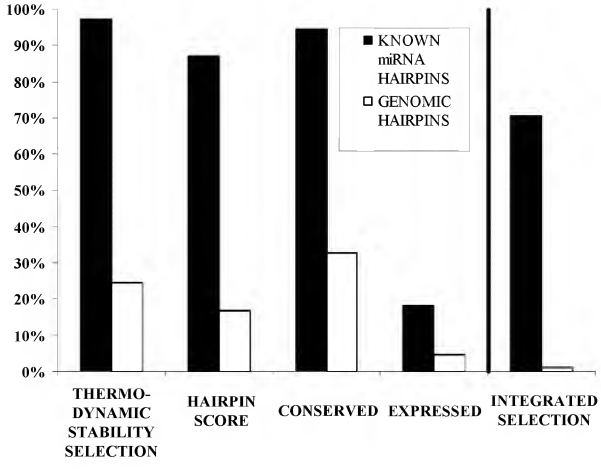

100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
KNOWN miRNA HAIRPINS
GENOMIC HAIRPINS
THERMO-DYNAMIC STABILITY SELECTION
HAIRPIN SCORE
CONSERVED
EXPRESSED
INTEGRATED SELECTION

FIG. 12B

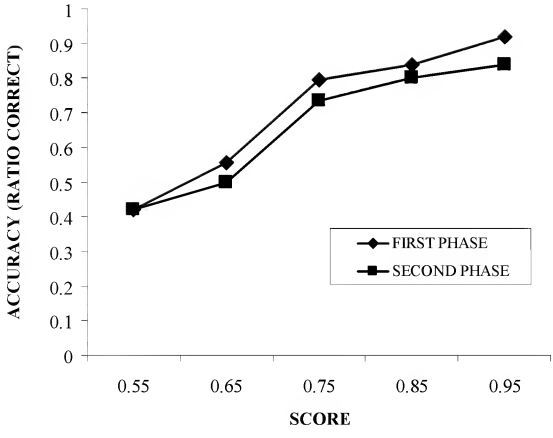

ACCURACY (RATIO CORRECT)
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0.55
0.65
0.75
0.85
0.95
SCORE
FIRST PHASE
SECOND PHASE

FIG. 12C

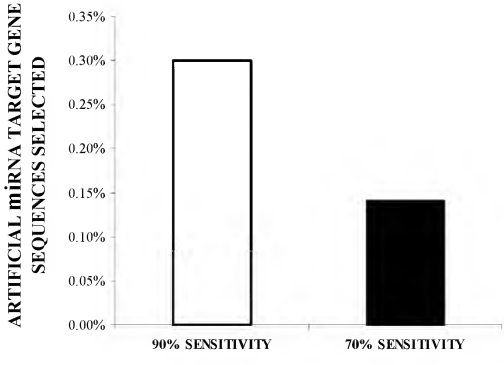

ARTIFICIAL miRNA TARGET GENE SEQUENCES SELECTED
0.35%
0.30%
0.25%
0.20%
0.15%
0.10%
0.05%
0.00%
90% SENSITIVITY
70% SENSITIVITY

FIG. 13

ROW	PRIMER SEQUENCE	SEQUENCED SEQENCE	PREDICTEDGAM RNA	DIST-ANCE	GAM NAME
1*	AATTGCTTGAAC	CCAGGAAGTGGA	AATTGCTTGAACCCAGGAAGTGGA	0	25-A
2*	ACTGCACTCC	AGCCTGGGC	ACTGCACTCCAGCCTGGGCTAC	0	351661-A
3	CACTGCACTC	CAGCCCGAGCAACA	CACTGCACTCCAGCCCGAGCAA	0	351946-A
4	CTAGACTGAAG	CTCCTTGAGGAC	CTAGACTGAAGCTCCTTGAGGA	0	352759-A
5	GAAGTTTGAAG	CCTGTTGTTCA	GAAGTTTGAAGCCTGTTGTTCA	0	4426-A
6	TCACTGCAAC	CTCCACCA	(TCACTGCAACCTCCACCACGTG),(TCACTGCAACCTCCACCAGCCT)	0	(357950-A),(352721-A)
7*	TCTAAGAGAAAG	GAAGTTCAGA	TCTAAGAGAAAGGAAGTTCAGA	0	337950-A
8	GGGCAGTGGA	GCTGGAA	GGGCGTGGAGCTGGAATGATGT	1	351996-A
9	AATTGCTTGAAC	CCAAGAAGTGGA	AATCACTTGAACCCAAGAAGTG	2	351874-A
10	AGCAGCCCA	GGGTTTTGT	AGCAAGACCAGGGTTTTGTGTT	2	352083-A
11	AGGCAAGACG	GACCAGA	AGGCAGAGAGGACCAGAGACT	2	351944-A
12	AGGGAAAGAAT	TAATGTGAA	GGGAAATAATTAATGTGAAGTC	2	353325-A
13	AGGGAAAGAAT	TAATGTGAG	AGGAAAAAAATTAATGTGAGTC	2	352649-A
14	ATTCAGTTG	CCCATGTTT	(ATTGTTGCCCATGTTTTTATTT),(TATTCATTGCCCATGTTTGTGA)	2	A),(352957-A,352960-A)
15	CTAGACTGAAG	CTCCTTGAGG	CTGGACTGAGCTCCTTGAGGCC	2	352288-A
16	TTCAGAGTGGT	TAAGTTCTG	TTCTGATGGTTAAGTTCTGTCA	2	353875-A
17	TTCAGAGTGGT	TAAGTTCTGC	TTCAAGTGTTTAAGTTCTGCTT	2	351940-A
18	AGCAGCCCA	GAAGGAAGC	AGGCCAAGAAGGAAGCAGAGG	3	352496-A
19	AGTTTGCCTTG	TAAGAAAAG	AGTTTGTGTAAGAAAAGC	3	352518-A
20	ATCAGAGGGTG	GGTGCTAA	ATTAGGAGAGTGGGTGCTAAGT	3	352511-A
21	ATGGTGGGAG	AGTTTGTCAGT	TGGAGGAGAGTTTGTCAGTATAG	3	353484-A
22	CCCAGGAAG	TGGAGCCTGGGC	CCCGGGTGGAGCCTGGGCTGTG	3	351990-A
23	GGGCAGTGGA	GGTCCGT	AGGGCAGGAGGTCCGTCCCTTC	3	353880-A
24	GGGCAGTGGA	TCTAGAC	GTGACAGTGAATCTAGACAGAC	3	352810-A
25	TCAAGCTCATTC	CACTAAA	CTCAGCTCATCCACTAAATCCC	3	353184-A
26	TGGAAAGTT	GGTTGTATGGTT	GGAATGGTGGTTGTATGGTTG	3	353855-A
27	TGGAGAGTT	CCATATTTTG	TGATAGATCCATATTTTGGTAA	3	352004-A
28	TGGAGAGTT	GTTTGTACAGT	TGGGTTTTGTTTGTACAGTGTA	3	353160-A
29	TCACTGCAAC	CTCCACC	TCACTGCAACCTCCACCTTCCG	0	353856-A

FIG. 14A

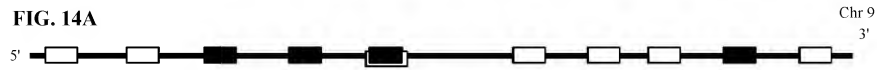


FIG. 14B

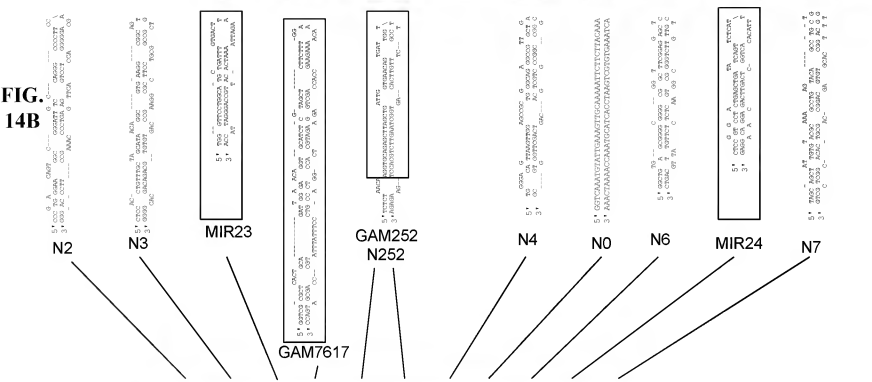


FIG. 14C

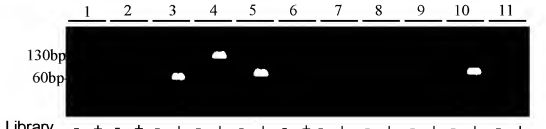
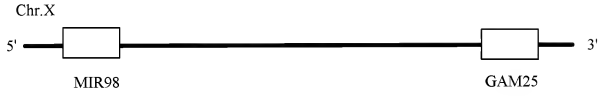


FIG. 15A

EST72223 (705 nt.)



EST72223 sequence:

CCCTTATTAGAGGATTCTGCTCATGCCAGGG**GTGAGGTAGTAAGTTGTATTG**
TTGTGGGGTAGGGATATTAGGCCCCAATTAGAAGATAACTATACAACT **MIR98**
TACTACTTTCCCTGGTGTGTGGCATATTCACACTTAGTCTTAGCAGTGTTGCC
TCCATCAGACAAAGTTGTAGATGTTCCTTGGATAATTTGGACTGGAAGAAAAGA
GACATGGAAGGGGACAGATGGTGTTTAGGGTGAGGCAGATGTCATTATAAAGT
GACTTGTCTTTCATTAATTGGAGCATATAATTATTTTACCTTTGGGCATGAACTC
ATTTTGCTATTCTTCAACTGTGTAATGATTGCATTTTATTAGTAATAGAACAGGA
ATGTGTGCAAGGGAATGGAAAGCATACTTTAAGAATTTGGGCCAGGCGCGGT
GGTTCATGCCTGTAATCCCAGCATTTTTGGGAGGCCGAGGCGGGTGGATCAC
CTGAGGTCAGGAGTTCGAGACCAACCTGGCCAACACGGCGAAACCCCGCCTC
TACTCAAATACAAAAATTAGCCAGGCTTGGTGACACTCGCCTGTGGTCCCAGC
TACTCAGGAGGCT**GAGGCAGGAG**AATTGCTTGAACCCAGGAAGTGGAG **GAM25**
GCTTCAGTGAGCTGAGAACACGCCACTGCACTCCAGTCCTGGGCAAC
AGAGCAAGACTCTGTCTCAGGAAAAAAAAAG

FIG. 15B

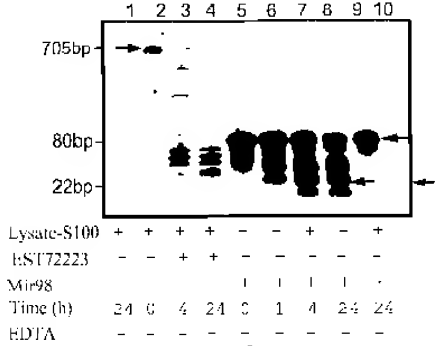
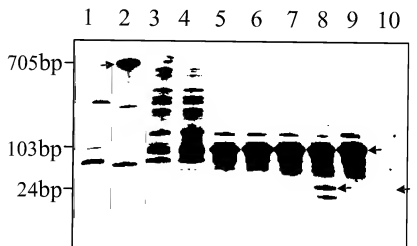
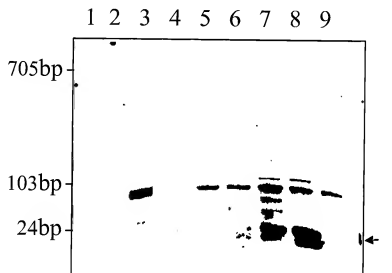


FIG. 15C



LYSATE-S100	+	+	+	+	+	+	+	+	+
EST72223	−	+	+	+	−	−	−	−	−
GAM25	−	−	−	−	+	+	+	+	+
TIME (H)	24	0	4	24	0	0.5	1	24	24
EDTA	−	−	−	−	−	−	−	−	+

FIG. 15D



LYSATE-S100	+	+	+	+	+	+	+	+	+
EST72223	−	+	+	+	−	−	−	−	−
GAM25	−	−	−	−	+	+	+	+	+
TIME (H)	24	0	4	24	0	0.5	1	24	24
EDTA	−	−	−	−	−	−	−	−	+

FIG. 16A

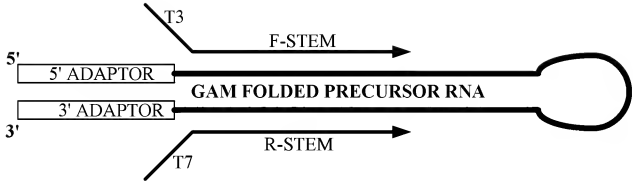


FIG. 16B

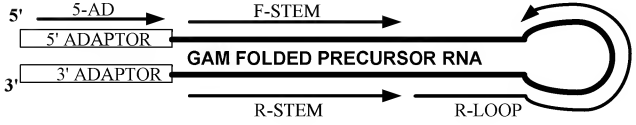


FIG. 16C

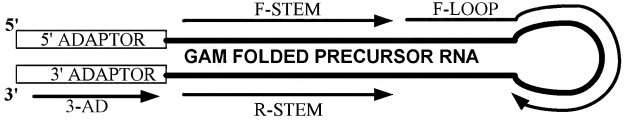


FIG. 17A

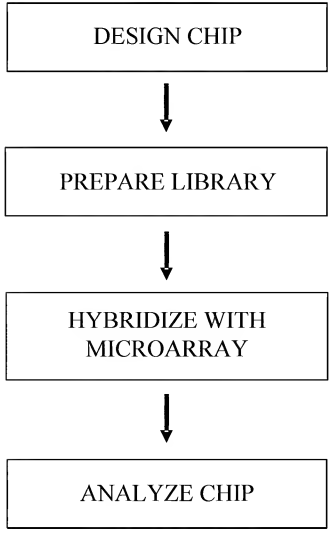

DESIGN CHIP
PREPARE LIBRARY
HYBRIDIZE WITH MICROARRAY
ANALYZE CHIP

FIG. 17B

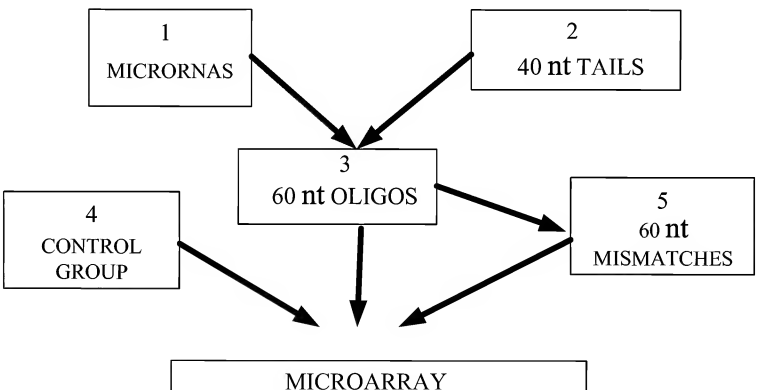

1
MICRORNAS
2
40 nt TAILS
3
60 nt OLIGOS
4
CONTROL
GROUP
5
60 nt
MISMATCHES
MICROARRAY

FIG. 17C

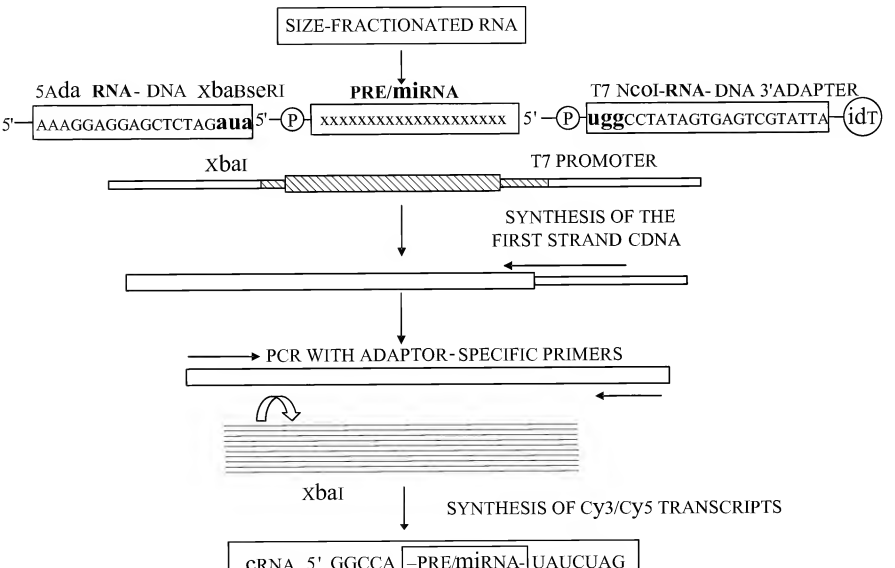

SIZE-FRACTIONATED RNA
5Ada RNA- DNA XbaBseRI
PRE/miRNA
T7 NcoI-RNA- DNA 3'ADAPTER
5'
AAAGGAGGAGCTCTAGaua
5'
P
xxxxxxxxxxxxxxxxxxxx
5'
P
uggCCTATAGTGAGTCGTATTA
idT
XbaI
T7 PROMOTER
SYNTHESIS OF THE
FIRST STRAND CDNA
PCR WITH ADAPTOR-SPECIFIC PRIMERS
XbaI
SYNTHESIS OF Cy3/Cy5 TRANSCRIPTS
cRNA 5' GGCCA –PRE/miRNA- UAUCUAG

FIG. 18A

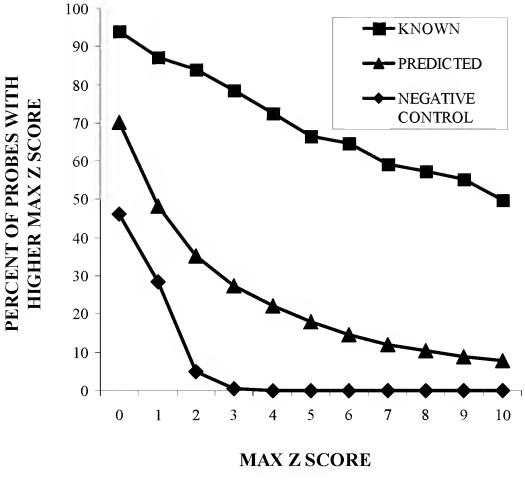

PERCENT OF PROBES WITH HIGHER MAX Z SCORE
100
90
80
70
60
50
40
30
20
10
0
0
1
2
3
4
5
6
7
8
9
10
MAX Z SCORE
KNOWN
PREDICTED
NEGATIVE CONTROL

FIG. 18B

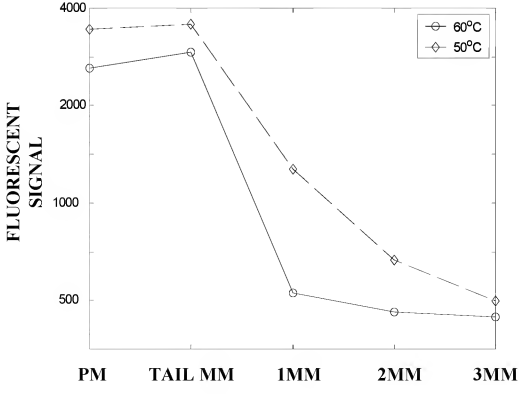

4000
2000
1000
500
FLUORESCENT SIGNAL
60°C
50°C
PM
TAIL MM
1MM
2MM
3MM

FIG. 18C

MIRNA NAME	HELA	BRAIN	LIVER	THYMUS	TESTES	PLACENTA	REFERENCE
HSA-MIR-124A	1879	**65517**	7025	3099	2672	2498	1,3
HSA-MIR-9	642	**42659**	3504	4455	4485	2313	2,3
HSA-MIR-128A	2015	**27701**	4940	4876	5166	2495	3
HSA-MIR-129	503	**22573**	1175	2213	5364	2017	3
HSA-MIR-128B	1168	**21969**	3954	4819	5383	2027	
HSA-MIR-122A	1051	447	**65518**	2644	617	570	1,3
HSA-MIR-194	501	910	**65518**	4737	2342	7952	3
HSA-MIR-148	413	620	**38436**	5250	6204	2711	
HSA-MIR-192	452	606	**20650**	1628	1263	2607	
HSA-MIR-96	887	3100	1477	**44800**	2266	5466	
HSA-MIR-150	648	1463	5295	**65518**	**29728**	5280	
HSA-MIR-205	551	615	1646	**65518**	2645	**39072**	
HSA-MIR-182	662	1944	1091	**25771**	2034	3683	
HSA-MIR-183	1026	1123	1286	**8754**	1681	2138	
HSA-MIR-204	525	3898	1757	6535	**64859**	6233	
HSA-MIR-10B	410	433	477	3871	**23083**	738	
HSA-MIR-154	438	733	1914	3309	**14750**	9637	
HSA-MIR-134	448	617	698	763	**2250**	997	
HSA-MIR-224	3233	11061	7684	**32305**	5377	**65518**	
HSA-MIR-210	844	2280	10703	6864	15288	**62452**	
HSA-MIR-221	625	9325	3520	**20212**	10608	**54287**	
HSA-MIR-141	696	805	1220	4063	2000	**46845**	
HSA-MIR-23A	1312	3492	2990	6021	11173	**40076**	
HSA-MIR-200C	556	595	1027	10636	1478	**33532**	
HSA-MIR-136	465	725	709	776	3100	**8840**	

1 LAGOS-QUINTANA ET AL., CURRENT BIOLOGY 12:735 (2002)

2 KRICHEVSKY ET AL., RNA 9:1274 (2003)

3 SEMPERE ET AL., GENOME BIOLOGY 5:R13 (2004)

FIG. 19A

5'UTR SEQUENCE (5' TO 3') OF HIV-1 (U5-R)

G<u>**GTCTCTCTGGTTAGACCAGATC**</u>**TGAGCCTGGGAGCTCTCTGGCTAACT**
AGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAAGTA
GTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTT
TTAGTCAGTGTGGAAAATCTCTAGCAGTGGCGCCCGAACAGGGACCTGAAAG
CGAAAGGGAAACCAGAGGAGCTCTCTCGA**CGCAGGACTCGGCTTGCTGAA**
GCGCGCACG<u>**GCAAGAGGCGAGGGGCG**</u>GCGACTGGTGAGTACGCCAAAAA
TTTTGACTAGCGGAGGCTAGAAGGAGAGAG

FIG. 19B

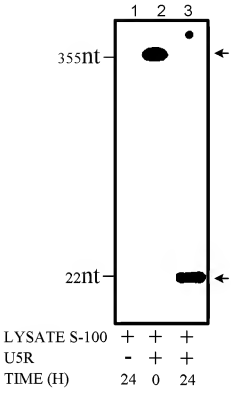


FIG. 19C

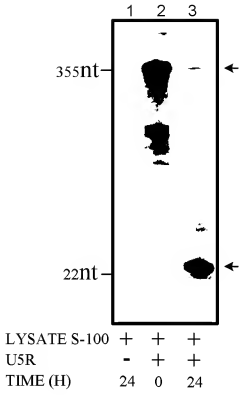
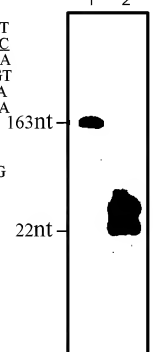


FIG. 19D

TRANSCRIPT SEQUENCE (5' TO 3')

ACAGGGCTGCTATTAACAAGAGAT
GGTGGTAATAGCAACAATGAGTCC
GAGATCTTCAGACCTGGAGGAGGA
GATATGAGGGACAATTGGAGAAGT
GAATTATATAAATATAAAGTAGTA
AAAATTGAACCATTAGGAGTAGCA
CCCACCAAGGCAAAGAGAA

GAM RNA:
TGAGTCCGAGATCTTCAGACCTGG



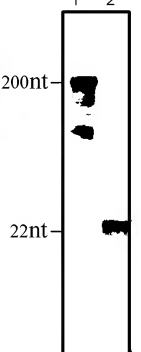
LYSATE S-100	+	+
TRANSCRIPT	+	+
TIME (H)	0	24

FIG. 19E

TRANSCRIPT SEQUENCE (5' TO 3')

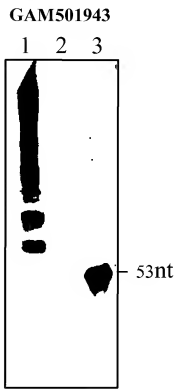
TGGGAAGCCCTCAAATATTGGTGG
AATCTCCTACAGTATTGGAGTCAG
GAACTAAAGAATAGTGCTGTTAGC
TTGCTCAATGCCACAGCCATAGCA
GTAGCTGAGGGGACAGATAGGGTT
ATAGAAGTAGTACAAGGAGCTTGT
AGAGCTATTCGCCACATACCTAGA
AGAATAAGACAGGGCTTGGAAAGG
ATTTTGCT

GAM RNA:
TGAGGGGACAGATAGGGTTATAGA



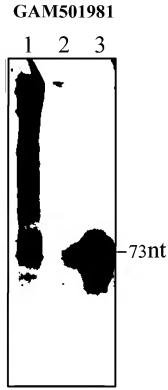
LYSATE S-100	+	+
TRANSCRIPT	+	+
TIME (H)	0	24

FIG. 20A



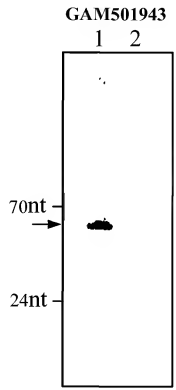
HELA	+	+	-
VACCINIA	+	-	-
GAM501943 TRANSCRIPT	-	-	+

FIG. 20B



HELA	+	+	-
VACCINIA	+	-	-
GAM501981 TRANSCRIPT	-	-	+

FIG. 20C



HELA	+	+
VACCINIA	+	-

FIG. 21A

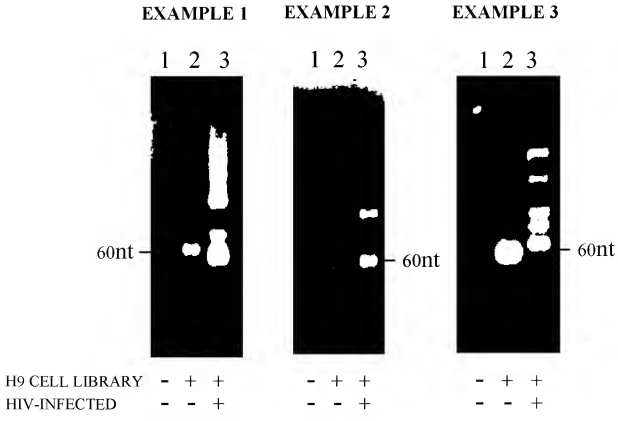

EXAMPLE 1
EXAMPLE 2
EXAMPLE 3
1 2 3
1 2 3
1 2 3
60nt
60nt
60nt
H9 CELL LIBRARY - + +
HIV-INFECTED - - +
- + +
- - +
- + +
- - +

FIG. 21B

ROW	PRIMER SEQUENCE	SEQUENCED SEQUENCE	GAM RNA SEQUENCE	GAM PRECURSOR			
				SEQUENCE	CHR	STRAND	START OFFSET
1	GGAAAGAAT	GGAAAGAATGTGGGTGCAC	GGAAAGGAAAGTGGGTGCAC	GACAGTGGCAATGGGGAAAGGAAAGTGGGTGCACTCAAGCTAGGCAGAAGTCAGCTAGGCAAGATGTGTAACTGGTTCAACTTCTGCATAGAGGAGAATGTAGGTCCTTTCCATTCTAATATAGATGTTC	11	+	6527398
2	GCAAGAGGCG	GCAAGAGGCGAGAAGCAGA	GCAAGAGTGAGAAGCAGA	CCCAGGTTCTGCAAGAGTGAGAAGCAGAAAGCCTACTTTGCGTTGCCTCTACCTGAGGAGAAGAAGCCAGGTGTGCTCTCAGATGGTCGGGGTAGTGCTTGGG	20	+	10164522
3	GGAAAGAAT	GGAAAGAATTAATGTGAG	GGAAAGGATAATGTGAG	ATTCTTCATGTTTGGCTAAAAGAGACTCCAACTGCTTGGCCTCTTTCTGAACCTACTATTAAGAGGAAAGGATAATGTGAGGCAGGCTAGTATGGACCTGTTTACTCCGATTTCATCAAATGGAGCTT	21	+	24398831
4	GGAAAGAAT	GGAAAGAATTAATGTGAA	GGAAAGATAATGTGAA	GCTAGAGAGTTGAGACCGAGTGAAGGCCACACCTCCGGAGGGAAAGATAATGTGAAGGCTCTCTCCACTGACATGTCACATGCTTTCTACTTGACTGGGCTTCCCTAAACTTGGGTAATTTTCAGC	6	+	50974009
5	CTTTTTGCCTG	CTTTTTGCCTGGGCAGGGC	CTTTTTGCAGGGCAGGGC	CTCTTCTAACTTCAGTCCTTTTTGCAGGGCAGGGCTTACTCTAGGAAACTTATTGCAAGGTAAGTCAAGTCCTTAAGGTCTGGCCACTCAGAG	5	-	65170275
6	CTCTCTGGT	CTCTCTGGTTAGTACTTGGA	CTAGTCTGGTTAGTACTTGGA	AGGGTCTAGTCTGGTTAGTACTTGGATGAGAGACCAAATAGCAAATACTTAAAATGTCTTTTCTAAGGAAATTAAATTGGCTCCT	11	+	88695685
7	GCAAGAGGCG	GCAAGAGGCGAGAAGCAGT	GCAGAGGCAGAAGCAGT	TCTTGCCTTGCACTGTCCATAAATCTGCCCTGGCTTTCTGCCTGACTGCACACTAAGAATCATGCACAGAAAGCAGAGGCAGAAGCAGTGATTGGTAAGG	1	+	193722202
8	CTCTCTGGTTTA	CTCTCTGGTTAGTAATAGG	CTCTCTGGAGAGTAATAGG	CTTTGAGAAAAAGAGGCTTGTTATATTCCAAGCATGAGATGATTATTAGAAACACTTATTTTCTGTTCTCTCTGGAGAGTAATAGGCAGAACCCCTTATCAGGG	2	-	240247210